# FIG.1a.

Synthetic DNA Substrates Mimicking Transcriptional Cis- Regulatory Elements

5' -GGGAATTCAAGGGGCGGGGCAAGGATCCAG -3' GC-box a:

5' -CTGGATCCTTGCCCCGCCCTTGAATTCCC -3'

GC-box b:

GC-box b MET: 5' -CTGGATCCTTGCCC <sup>m</sup>CGCCCCTTGAATTCCC -3'

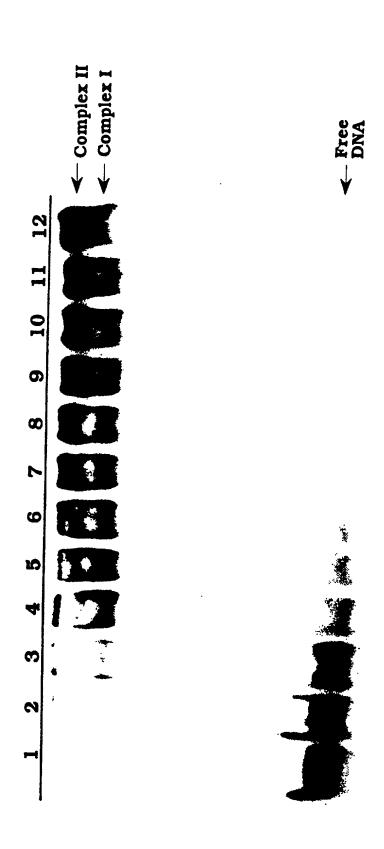
5' -GGGAATTCAAATGACGTCAAAAGGATCCAG -3' 5' -CTGGATCCTTTTGACGTCATTTGAATTCCC -3' CRE b: CRE a:

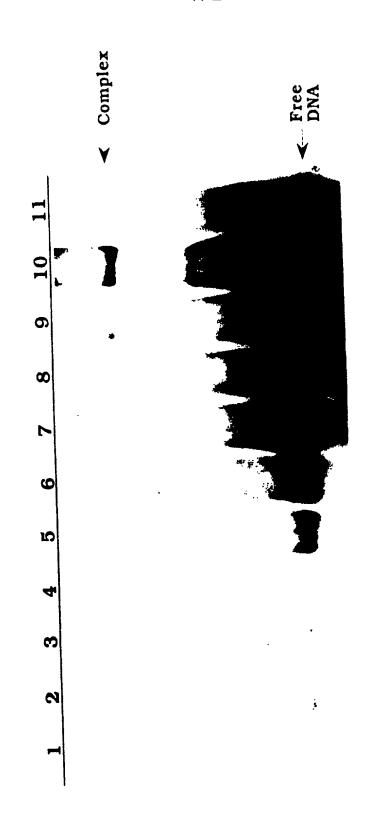
5' -GGGAATTCAAATGA<sup>M</sup> CGTCAAAAGGATCCAG -3' CRE a MET:

# FIG. 1

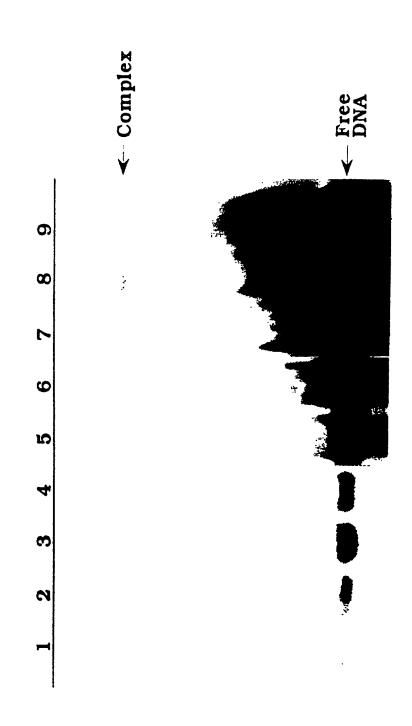
			2/26				
Kii IC50 (nM) (nM)	8	20 15	S.	30	20	150	300
Vα	0089		G	CAACCCTCCAC-3'			·6-5
Sequence	5'-CTGGATCCTTGCCCCGCCCCTTGAATTCCC-3	5'-CTGGATCCTTGCCCmCGCCCCTTGAATTCCC-3'	5'-CTGGATCCTTGCCCmCGCCCCTTGAATTCCC-3'	5'- CCTACCCACCCTGGATCCTTGCCCmCGCCCCTTGAATTCCCAACCCTCCAC-3'	5'-ATCCTTGCCCmCGCCCCTTGAAT-3'	5'TTGCCCmCGCCCTT-3'	5'-GGGAATTCAAATGAmCGTCAAAAGGATCCAG-3'
NUCLEO- TIDES	30	30	30	50 5'-	22	4	30
NAME NC TIE	GC-Box b	GC-Box bMET (SEQ ID NO: 10)	GC BoxpMET (SEQ ID NO: 10)	GC-Box cMET	(SEQ ID NO: 13) GC Box dMET (SEQ ID NO: 14)	GC-Box eMET (SEQ ID NO: 15)	CRE aMET (SEQ ID NO: 11)



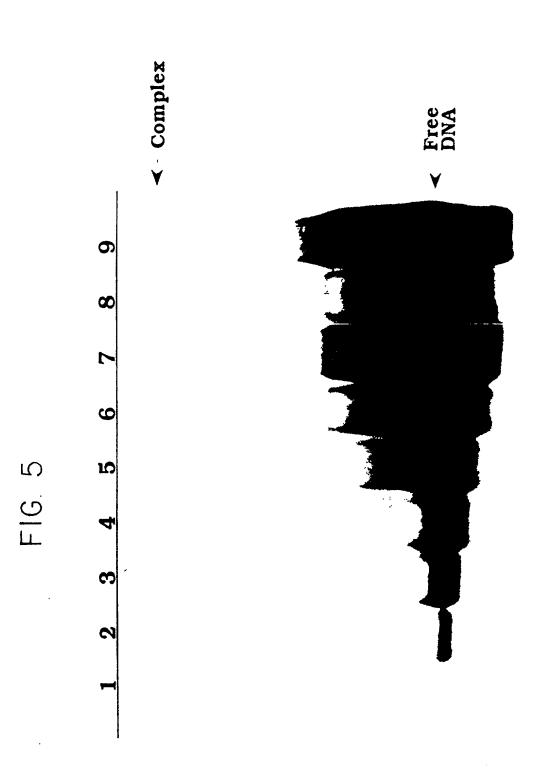












Primer D

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### FIG.7a.

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#### STARTING POPULATION

## FIG.7b. GENERATION 1

### FIG.7c. GENERATION 3

## 1G.7d.

3pT G#	_	5	6	6	&	<b>∞</b>	&	7	7		. 9	6 10	9 0 6
TpG GpT	•	•	•	•	•	•	•	•	•		•	•	
GENERATION 5	TGGGGGGGGGCGGGGGGAGTTTGA	GGGGGGAGGGCGGATAGTTGTGTG	GGGTGGGGTGGGGTGTGGG	GAGGGGGGGAGCGGAGGGGGTTGGG	GGGGGGAAGGGCGTGGGGTTGGGTG	-GGGAGGGGGGCGATGGGGTGGTGG	GGGTGGGGTGGCGTTGTGGGTGGGG	GGGAGGGGTGGCGGTGGGTATGTGG	GGGGAGGGTGGCGGGTATGGAGTGG		GGGGGGGAGTGCGTTGATGGGTGTG	GGGGGGGAGTG <u>CG</u> TTGATGGGTGTG GGGGGGTGGAT <u>CG</u> TGGGGGGGGGG	GGGGGGGAGTGCGTTGATGGGTGTG GGGGGGGGGGGGGG
TpG	•		•				•	•	•		•	• •	• • •
GpT			•				•	•	•		•	• •	• • •
#5	7	=	10	10	10	10	10	10	10	•	20	10 9	0 0

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# FIG. 7e.

#5	2	9	7	9	9	5	9	7	6	0	ω	œ
TpG GpT	•		•	•	•	•		•	•	•	•	•
TpG	•	•	•	•	•	•	•	•	•	•	•	•
GENERATION 5	GGGAGGGGTAGCGGGAGTGTGTG	GGGGGTAAGGGGGG	GGGGGGTGGTTCGGTAATGGGGGGT	GGTGGGAGAGGCGTGGTGTAGGTAG	GGGGGGGTGTACGAGGTTTGTGTGG	TGGTGGAGGGGCGAAGAGTGTGTG	GGGGGTGGGATGCGGAATAAGGATGG	TGAGGGGAGGCGAATAGATGGTGG	GGGGGGAGTAAGCGGGGGGTGTGGTGG	TGAAGGGGGGTGCGGGGGG-	GTGGTGATGGGGCGGGGGTGGTGG	TGGAGGGGTAGGCGTGGGGTGATGGG
TpG			•	•	•	•	•	•		•	•	•
GpT	•	•	•	•	•	•	•		•	•	•	•
<b>#</b> 5	6	6	တ	တ	တ	တ	တ	တ	∞	∞	ω (	∞

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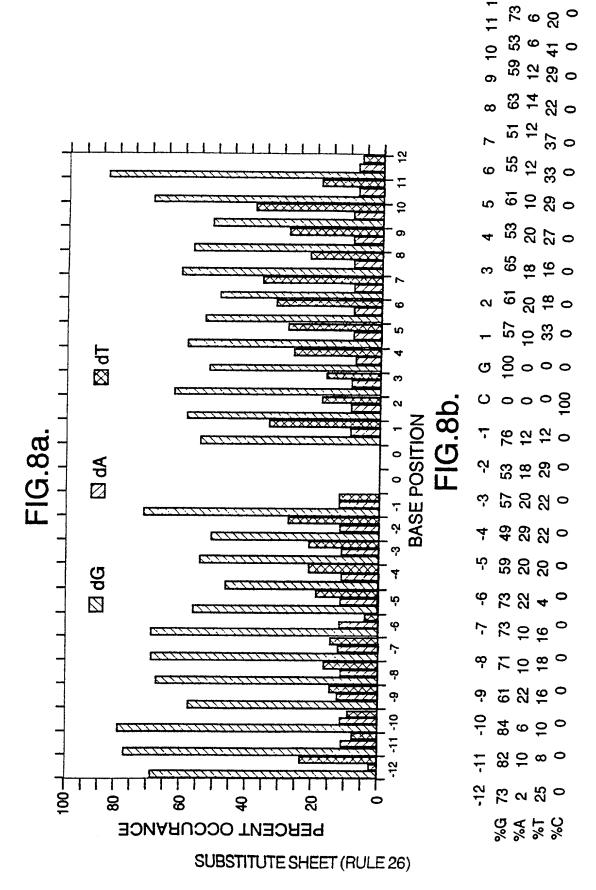
FIG. 7f.

<b>#</b> 5	ω	∞	7	9	9	10	တ	တ	တ	∞	ω	7
Тра срт	•	•	•	•	•	•	•	•	•	•	•	•
	GTGATGGG	<b>3TAGAGGGG</b>	rgtgtggg •••	GTATGTAG	GTGGTGGG ••	GGGGTTGG .	FTGGGGGGG ••	BATGGGGTG	GTGGGGG .	GGGGGTGG ••	GGTGGTGG	TGTGATGG
GENERATION 5	GGTAGGGAGTGGCGGGTGGTGATGGG	GGGTGTAGAGGCCGGGAGTAGAGGGG	GGGTGGGTTTGGCGTAATTGTGTGGG	GGGTGTGTTGGGCGTGGGGGTATGTAG	TGGGGAGAATGGCGGGGGGGTGGTGGG	TATGGTGGGAGGCGGGGGGGGTTGG	TGGGGAAAGAGGCGTGAGTGGGGGGG	TGTAGGGGAGGACGGGGGGGTG	GGGTGGGTAATGCGTAGGGTGGGGGG	GTGTGGGTAAGGCGGTATGGGGGTGG	TGGAGGGTGTTGCGGTGAGGTGGTGG	GGTGGTGATCGGGGTTGTGATGG
TpG	•	•	•	•	•	•	•	•	•	•	•	•
GpT	•	•	•	:		•		•	•	•	:	•
<b>#</b> 5	∞	ω	ω	∞	_	7	7	7	7	7	7	7

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Ğ	/	7	7	7	9	2	ω	9	9	4	10	0
TpG GpT	:	•	•	•	•		•	:	•	•	•	
TpG	•	•	•	:	•	•	•	•	•	•	•	•
GENERATION 5	GGGGGTAAAGTGCGGGTGGTTGATGG	GTGGAGGTGTTGCGTAGTGTGGGAGG	GTGGGGAATGGTCGGTTATGGTGGGG	GGGATGTGGTAGCGGGGGTGTGTTAG	GGGGTAGGAGTTCGTAGGGGTGTGTT	GAGGTGGTGGATCGGGATGATGGATT	TGGGGGGAAATACGGGGGGGGGGTGGTA	GGAGTAGGGTTACGTGGTGGTAATGG	GAGGAGTAAAGGCGTGTGTTGTGGTG	TGGATGAGAGTGCGTGTATGATAAGG	<b>AGGGTTAGTGAACGGGGGGGGGGGTGG</b>	GAGAAGGGTAAACCTGGGGGGGGGA
TpG	•	•	•	•		•	•			•	•	
GpT	•	•	•	•	•	•	•	•	•	•	•	•
#5	7	7	7	7	7	/	9	9	9	9	2	2

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FIG.9a

The first of the first will again to make the first of th

DEFINITION Lyt-2.2 gene, T- cell differentiation antigen, 3' UTR. ACCESSION GB\_RO:MMLYT22

TGGGGGGGGGGGGGGGGGGGTTTGA

GAACAATGGGGGGGGGGGGGGGGGGGGTTTAGCTATGTCAGAATTCA 5100

5110

5120

5130

5140

DEFINITION homeo box 2.6 (Hox-2.6) mRNA ACCESSION GB\_RO:MUSHOX26

86

880

870

8

910

920

DEFINITION growth arrest-specific promoter gene, gas-1 ACCESSION GB\_RO:MMGAS1PRA

2510

15/26

DEFINITION pim-1 proto-oncogene, pim-1 protein kinase, CpG island, 5' UTR region.
ACCESSION GB\_RO:MUSPIM1

The second states that the transition of the second states that the second states the second states that the second states that the second states the second states the second states the second states that the second states the second s

GAGGGGGGGAGCGGAGGGGGTTGGG

GAGGGGTGTAGCCGCGAGGGGGGGGGGGGGGGGGGGGCCCTGGTCCCGCCGCC 1500

1510

1540

1530

1520

DEFINITION neuronal dihydropyridine-sensitive L-type calcium channel alpha-1 subunit mRNA, 3' UTR. ACCESSION GB\_RO:MUSDHPCC

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FIG.9c.

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**HUMAN SEQUENCES** 

Huntington's Disease Region, chromsome 4p16.3. GB\_PR:HSL1C2 DEFINITION

**ACCESSION** 

Human Down Syndrome region of chomosome 21. DEFINITION

GB\_HTG:HSAC000002 ACCESSION

DEFINITION

upstream region of HoxA7 gene, CpG island. ACCESSION

GB\_PR:HSHCRDNA

chromosome 22 CpG island DNA DEFINITION

GB\_PR:HS303B3 **ACCESSION** 

DEFINITION

CpG island DNA. GB\_PR:HS167B9F **ACCESSION** 

Y chromosome sex determining region, Yp pseudoautosomal DEFINITION

boundary, PAB1

GB\_PR:HSCAMF3X1 ACCESSION

creatine transporter and paralogous genes, pericentomeric DEFINITION

repeats on chromosome 16.

GB\_PR:HSU41302 ACCESSION

cathepsin D (cat D) gene, exon 5. GB\_PR:HUMCATD3 DEFINITION

ACCESSION

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:

argininosuccinate synthetase gene 5' end, CpG island DEFINITION

GB\_PR:HSASG5E ACCESSION

**DEFINITION**ACCESSION

argininosuccinate synthetase gene 5' end, CpG island GB\_PR:HUMAS1

vimentin gene, 5' regulatory region, CpG island. GB\_PR:HUMVIM DEFINITION **ACCESSION** 

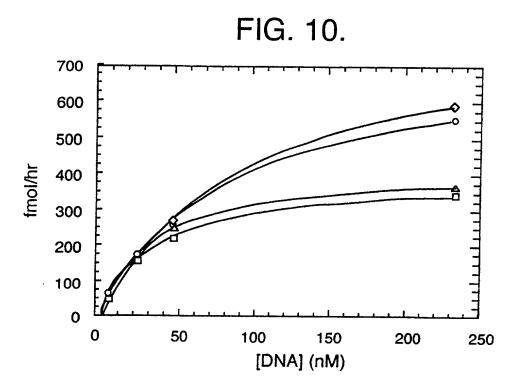
vimentin gene, exon 1, 5' end CpG island. GB\_PR:HUMVIM02 DEFINITION **ACCESSION** 

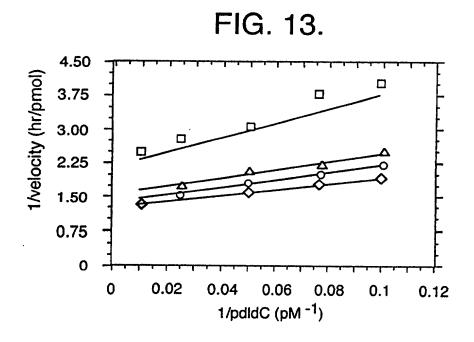
vimentin gene, 5' end, CpG island. GB\_PR:HUMVIMAA DEFINITION

**ACCESSION** 

vimentin gene, 5' end, CpG island GB\_PR:HSVIM5RR **DEFINITION ACCESSION** 

**DEFINITION**ACCESSION





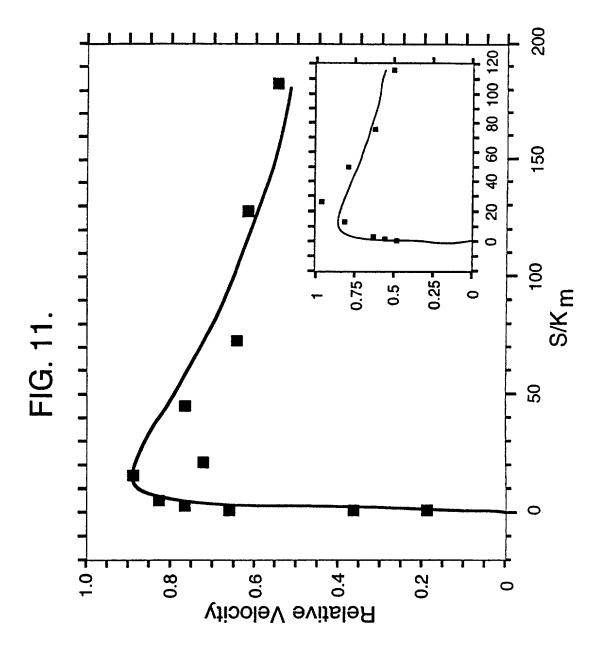


FIG.12a.

2.0

1.5

1.5

0.0

0.02

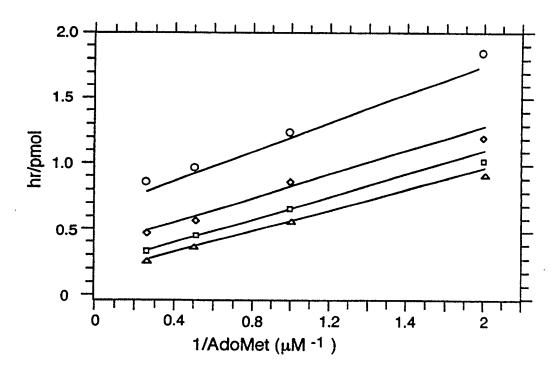
0.04

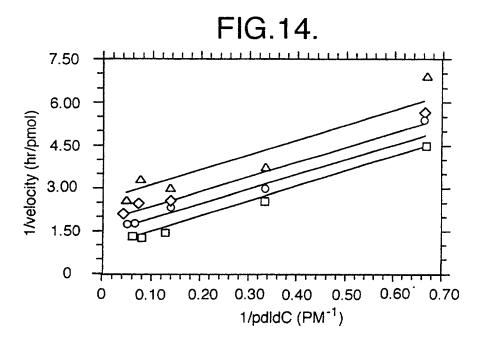
0.06

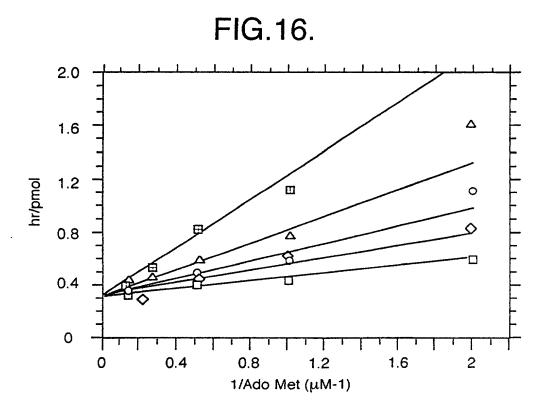
0.08

1/pdldC (p M<sup>-1</sup>)

FIG.12b.







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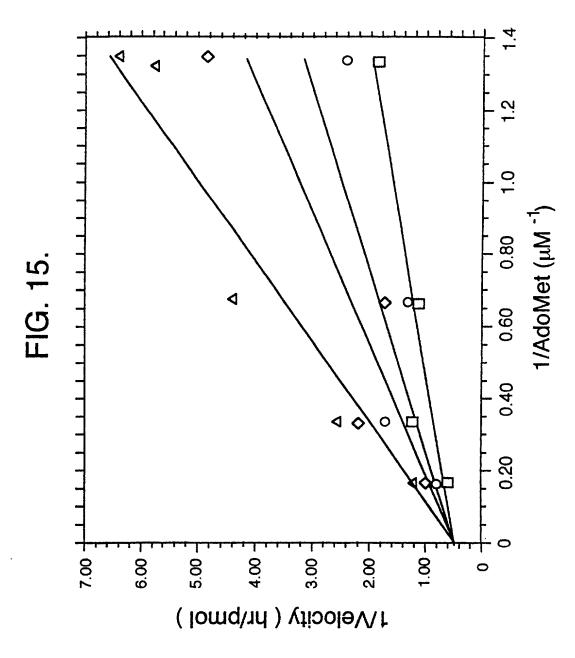


FIG. 17a.

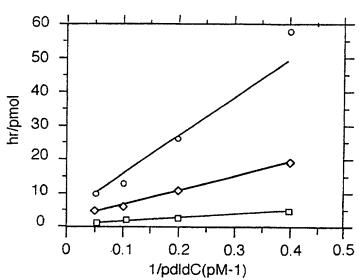


FIG. 17b.

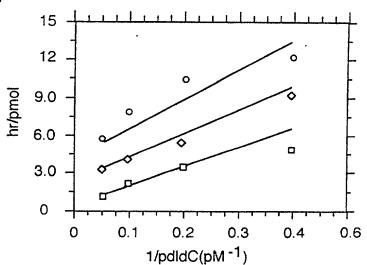
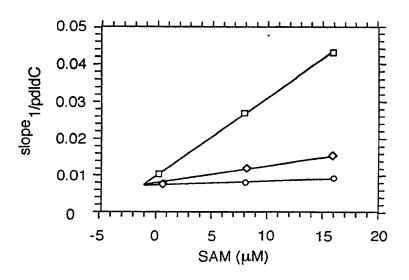


FIG. 17c.



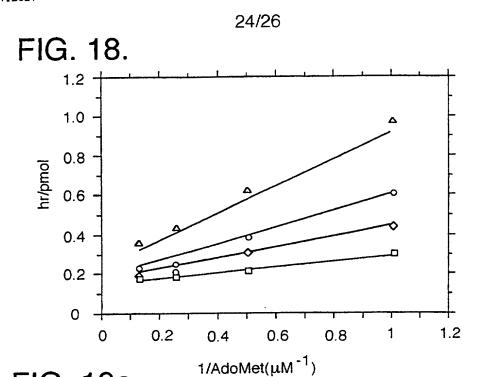


FIG. 19a.

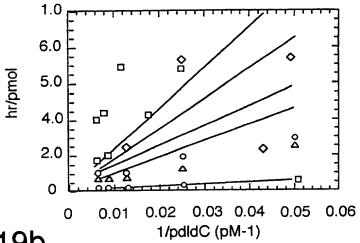
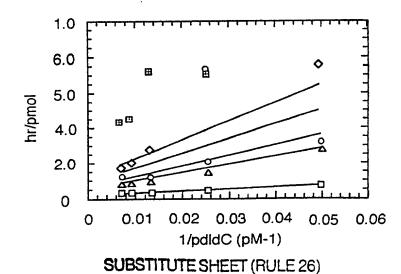


FIG. 19b.



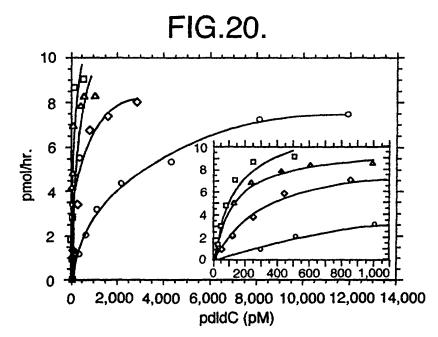


FIG.21.

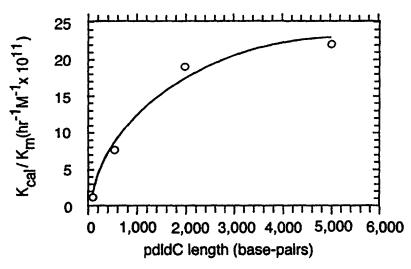


FIG.22.



FIG.23a.

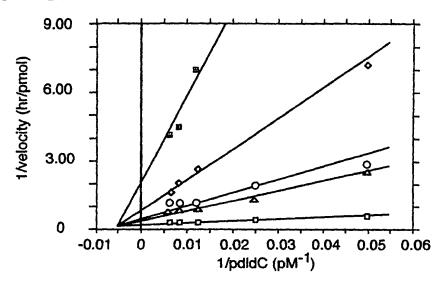


FIG.23b.

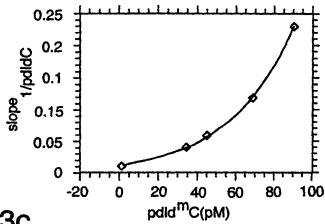
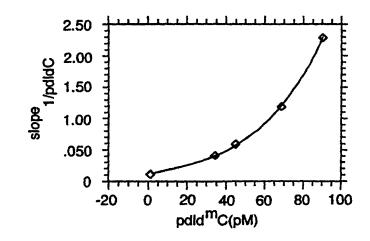


FIG.23c.



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